

### **AMENDMENTS TO THE SPECIFICATION**

Please amend the specification as follows:

**Paragraph at page 4, lines 11-18:**

~~Figure 2 shows~~ Figures 1A, 1B and 1C show a comparison of the amino acid sequences of the UDP-glucose 4-epimerase from soybean clone sls2c.pk017.k22: fis (SEQ ID NO:14), wheat clone wdk5c.pk006.o4: fis (SEQ ID NO:16), corn clone cen3n.pk0155.b8: fis (SEQ ID NO:18), rice clone rlr2.pk0043.c3: fis (SEQ ID NO:20), soybean clone se6.pk0014.f12 (SEQ ID NO:22), *Pisum sativum* (NCBI General Identifier No. 1173555, SEQ ID NO:25) and *Cyamopsis tetragonoloba* (NCBI General Identifier No. 3021357, SEQ ID NO:26). Amino acids conserved among all sequences are indicated by an asterisk (\*) above the alignment. Dashes are used by the program to maximize the alignment.

**Paragraph at page 20, lines 19-27:**

~~Figure 1 presents~~ Figures 1A, 1B and 1C present an alignment of the amino acid sequences set forth in SEQ ID NOs:14, 16, 18, and 22 and the *Pisum sativum* and *Cyamopsis tetragonoloba* sequences (SEQ ID NO:25 and SEQ ID NO:26). The amino acid sequence from clone cen3n.pk0155.b8: fis contains 353 amino acids and the amino acid sequence from *Cyamopsis tetragonoloba* contains 350 amino acids, but the alignment between both sequences starts at amino acid 65 of the *Cyamopsis tetragonoloba* sequence. The data in Table 6 represents a calculation of the percent identity of the amino acid sequences set forth in SEQ ID NOs:2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, and 24 and the *Pisum sativum* and *Cyamopsis tetragonoloba* sequences (SEQ ID NO:25 and SEQ ID NO:26).